

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Fred Hutchinson Cancer Research Center, Inc.
 (B) STREET: 1100 Fairview Avenue North, Mailstop c2M-027
 (C) CITY: Seattle
 (D) STATE: Washington
 (E) COUNTRY: USA
 (F) POSTAL CODE (ZIP): 98109

(A) NAME: Thomas Spies
 (B) STREET: 2429 E. Aloha
 (C) CITY: Seattle
 (D) STATE: Washington
 (E) COUNTRY: USA
 (F) POSTAL CODE (ZIP): 98112

(A) NAME: Veronika Spies
 (B) STREET: 2429 E. Aloha
 (C) CITY: Seattle
 (D) STATE: Washington
 (E) COUNTRY: USA
 (F) POSTAL CODE (ZIP): 98112

(ii) TITLE OF INVENTION: CELL STRESS REGULATED HUMAN MHC CLASS I GENE

(iii) NUMBER OF SEQUENCES: 16

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/029,044
 (B) FILING DATE: 29-OCT-1996

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11722 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CACTGCTTGA GCCGCTGAGA GGGTGGCGAC GTCGGGGCCA TGGGGCTGGG CCCGGTCTTC	60
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TCCTGGCGGT CCTCGGCGGA GCGGGAGCAG TGGGACGTTT CCGGGGGTCG GGTGGGTAGC	180
GGCGAGCGCT GTGCGGTCAG GGCGGGGCTC CTGTGCCCTG TCGGTGGCGC AGGGAGCTGG	240

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GGATCGCGCA	TCACCTGCAC	TTTCTGGTCT	CCTCCTGCTC	TTTCTCTCCT	CGCGTCTCCT	360
CCGCTTCCTC	TCACTTTTTCG	GACAAACCAG	TCCTTCTGAG	GCCCATGGGT	TCCCCGGGCTG	420
CCTCCGGGGC	TGCTCCTGTG	AATGGCATTG	GAGTGCCCTT	CCAGCGCGGC	CACTGAAGCA	480
GCCACAACCC	CCGGTGCTCG	GGGCGGCTCT	CAGGTCCCTG	AAGTCCTGTC	CTCTCCCGGA	540
GCCGACGTGT	TCTCAGCTCC	TGGGCCGCGAG	CTCCTGGAGT	AGGGGCCCTC	CTTTCTCGGG	600
ACCCGGAGCT	GGTGCTTCCT	GCTGCTGTGG	GGACTGTGGG	GGGTCCTGAC	TCTCAAGCTG	660
AGGGGTGGGA	GTCTGCAGGC	TCCGGGCAGA	GGATTCTTCC	TGCGACTTCT	CTCATCCCCA	720
GCTCATTCTC	CCCTCGCCTC	TGGCTCCGAG	GGTCCTCTCC	TCTCTCTCAT	CCCACCCCTA	780
CTAATGACCA	GTGATCTAAG	GACACCAGAT	TCCCTCTCAC	CTCCTCCCTG	CCCATCTCAG	840
GGCCCCTGA	GTCCTTTTCG	CCTCCAGCT	CCCTGCTACC	CCTTCCTGTG	TGCTGTTCTC	900
TGATCCATTT	CTAGGGTGTC	CTCTGCCCTC	ATCCCCTGTC	CCCGCCACCG	AAGTCCCTCC	960
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CCTTAGGCAG	GGCGCAGGGC	AGCGCAGATG	CCCCCTCCCC	TCCAGTGCGAG	ATGCCTGTTC	1200
TGGACCCTGC	CTCATTGTGG	CCCCTTCCCC	ACTCCTTCAT	CCTCAGCCTC	ACCCTCTTGA	1260
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TCCCTGCTCC	CCCAC'TCCCC	ACTACCCTTC	TCAGCCTCTG	GTAATCATCA	TTCTATTGTC	2160
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AAATGACACG	ATGGCTGAAT	AGTTCTCCAC	ATACACATGT	ACACCACATT	TTCTTTATCC	2340
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GGGGTCAGTG	GAACCTCAGCA	GGGAGGTGAG	CCGGCACTCA	GCCCACACAG	GGAGGCATGG	7380
GGGAGGGCCA	GGGAGGCGTA	CCCCCTGGGC	TGAGTTCCTC	ACTTGGGTGG	AAAGGTGATG	7440
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CAGACATTCC	ATGTTTCTGC	TGTTGCTGCT	GCTGCTGCTG	CTATTTTGTG	TATTATTATT	8820
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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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Ala	Pro	Pro	Gly	Ala	Ala	Ala	Glu	Pro	His	Ser	Leu	Arg	Tyr	Asn	Leu
			20				25					30			
Thr	Val	Leu	Ser	Trp	Asp	Gly	Ser	Val	Gln	Ser	Gly	Phe	Leu	Ala	Glu
		35				40					45				

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Val His Leu Asp Gly Gln Pro Phe Leu Arg Tyr Asp Arg Gln Lys Cys
 50 55 60
 Arg Ala Lys Pro Gln Gly Gln Trp Ala Glu Asp Val Leu Gly Asn Lys
 65 70 75 80
 Thr Trp Asp Arg Glu Thr Arg Asp Leu Thr Gly Asn Gly Lys Asp Leu
 85 90 95
 Arg Met Thr Leu Ala His Ile Lys Asp Gln Lys Glu Gly Leu His Ser
 100 105 110
 Leu Gln Glu Ile Arg Val Cys Glu Ile His Glu Asp Asn Ser Thr Arg
 115 120 125
 Ser Ser Gln His Phe Tyr Tyr Asp Gly Glu Leu Phe Leu Ser Gln Asn
 130 135 140
 Val Glu Thr Glu Glu Trp Thr Val Pro Gln Ser Ser Arg Ala Gln Thr
 145 150 155 160
 Leu Ala Met Asn Val Arg Asn Phe Leu Lys Glu Asp Ala Met Lys Thr
 165 170 175
 Lys Thr His Tyr His Ala Met His Ala Asp Cys Leu Gln Glu Leu Arg
 180 185 190
 Arg Tyr Leu Glu Ser Ser Val Val Leu Arg Arg Arg Val Pro Pro Met
 195 200 205
 Val Asn Val Thr Arg Ser Glu Ala Ser Glu Gly Asn Ile Thr Val Thr
 210 215 220
 Cys Arg Ala Ser Ser Phe Tyr Pro Arg Asn Ile Thr Leu Thr Trp Arg
 225 230 235 240
 Gln Asp Gly Val Ser Leu Ser His Asp Thr Gln Gln Trp Gly Asp Val
 245 250 255
 Leu Pro Asp Gly Asn Gly Thr Tyr Gln Thr Trp Val Ala Thr Arg Ile
 260 265 270
 Cys Gln Gly Glu Glu Gln Arg Phe Thr Cys Tyr Met Glu His Ser Gly
 275 280 285
 Asn His Ser Thr His Pro Val Pro Ser Gly Lys Val Leu Val Leu Gln
 290 295 300
 Ser His Trp Gln Thr Phe His Val Ser Ala Val Ala Ala Ala Ala Ala
 305 310 315 320
 Ala Ile Phe Val Ile Ile Ile Phe Tyr Val Arg Cys Cys Lys Lys Lys
 325 330 335
 Thr Ser Ala Ala Glu Gly Pro Glu Leu Val Ser Leu Gln Val Leu Asp
 340 345 350

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Gln His Pro Val Gly Thr Ser Asp His Arg Asp Ala Thr Gln Leu Gly
 355 360 365

Phe Gln Pro Leu Met Ser Ala Leu Gly Ser Thr Gly Ser Thr Glu Gly
 370 375 380

Ala
 385

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGGCCATGGG GCTGGGCCGG GTCCTGCTGT TTCTGGCCGT CGCCTTCCCT TTTGCACCCC	60
CGGCAGCCGC CGCTGAGCCC CACAGTCTTC GTTACAACCT CATGGTGCTG TCCCAGGATG	120
AATCTGTGCA GTCAGGGTTT CTCGCTGAGG GACATCTGGA TGGTCAGCCC TTCCTGCGCT	180
ATGACAGGCA GAAACGCAGG GCAAAGCCCC AGGGACAGTG GGCAGAAGAT GTCCTGGGAG	240
CTAAGACCTG GGACACAGAG ACCGAGGACT TGACAGAGAA TGGGCAAGAC CTCAGGAGGA	300
CCCTGACTCA TATCAAGGAC CAGAAAGGAG GCTTGCATTC CCTCCAGGAG ATTAGGGTCT	360
GTGAGATCCA TGAAGACAGC AGCACCAGGG GCTCCCGGCA TTTCTACTAC GATGGGGAGC	420
TCTTCCTCTC CAAAACCTG GAGACTCAAG AATCGACAGT GCCCCAGTCC TCCAGAGCTC	480
AGACCTTGGC TATGAACGTC ACAAATTTCT GGAAGGAAGA TGCCATGAAG ACCAAGACAC	540
ACTATCGCGC TATGCAGGCA GACTGCCTGC AGAAACTACA GCGATATCTG AAATCCGGGG	600
TGGCCATCAG GAGAACAGTG CCCCCATGG TGAATGTCAC CTGCAGCGAG GTCTCAGAGG	660
GCAACATCAC CGTGACATGC AGGGCTTCCA GCTTCTATCC CCGGAATATC AACTGACCT	720
GGCGTCAGGA TGGGGTATCT TTGAGCCACA ACACCCAGCA GTGGGGGGAT GTCCTGCCTG	780
ATGGGAATGG AACCTACCAG ACCTGGGTGG CCACCAGGAT TCGCCAAGGA GAGGAGCAGA	840
GGTTCACCTG CTACATGGAA CACAGCGGGA ATCACGGCAC TCACCCTGTG CCCTCTGGGA	900
AGGTGCTGGT GCTTCAGAGT CAACGGACAG ACTTTCCATA TGTTTCTGCT GCTATGCCAT	960
GTTTTGTAT TATTATTATT CTCTGTGTCC CTGTGTGCAA GAAGAAAACA TCAGCGGCAG	1020
AGGGTCCAGA GCTTGTGAGC CTGCAGGTCC TGGATCAACA CCCAGTTGGG ACAGGAGACC	1080
ACAGGGATGC AGCACAGCTG GGATTTGAGC CTCTGATGTC AGCTACTGGG TCCACTGGTT	1140

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CCACTGAGGG CGCCTAGACT CTACAGCCAG GCGGCCAGGA TTCAACTCCC TGCCTGGATC 1200
 TCACCAGCAC TTTCCCTCTG TTTCTGACC TATGAAACAG AAAATAACAT CACTTATTTA 1260
 TTGTTGTTGG ATGCTGCAAA GTGTTAGTAG GTATGAGGTG TTTGCTGCTC TGCCACGTAG 1320
 AGAGCCAGCA AAGGGATCAT GACCAACTCA ACATTCCATT GGAGGCTATA TGATCAAACA 1380
 GCAAATTGTT TATCATGAAT GCAGGATGTG GGCAAACCTCA CGACTGCTCC TGCCAACAGA 1440
 AGGTTTGCTG AGGGCATTCA CTCCATGGTG CTCATTGGAG TTATCTACTG GGTCACTCTAG 1500
 AGCCTATTGT TTGAGGAATG CAGTCTTACA AGCCTACTCT GGACCCAGCA GCTGACTCCT 1560
 TCTTCCACCC CTCTTCTTGC TATCTCCTAT ACCAATAAAT ACGAAGGGCT GTGGAAGATC 1620
 AGAGCCCTTG TTCACGAGAA GCAAGAAGCC CCCTGACCCC TTGTTCCAAA TATACTCTTT 1680
 TGTCTTTCTC TTTATTCCCA CGTTCGCCCT TTGTTGAGTC CAATACAGGG TTGTGGGGCC 1740
 CTTAACAGTG CCATATTAAT TGGTATCATT ATTTCTGTTG TTTTGTGTTT TGTGTTTGTGTT 1800
 TTTGTTTTTG AGACAGAGTC TCACTCGTCA CCCAGGCTGC AGTTCACTGG TGTGATCTCA 1860
 GCTCACTGCA ACCTCTGCCT CCCAGGTTCA AGCACTTCTC GTACCTCAGA CTCCCGATAG 1920
 CTGGGATTAC AGACAGGCAC CACCACACCC AGCTAATTTT TGTATTTTTT GTAGAGACGG 1980
 GGTTCGCCA AGTTGACCAG CCCAGTTTCA AACTCCTGAC CTCAGGTGAT CTGCCTGCCT 2040
 TGGCATCCCA AAGTGCTGGG ATTACAAGAA TGAGCCACCG TGCCTGGCCT ATTTTATTAT 2100
 ATTGTAATAT ATTTTATTAT ATTAGCCACC ATGCCTGTCC TATTTTCTTA TGTTTTAATA 2160
 TATTTTAATA TATTACATGT GCAGTAATTA GATTATCATG GGTGAACTTT ATGAGTGAGT 2220
 ATCTTGGTGA TGA CTCTCC TGACCAGCCC AGGACCAGCT TTCTTGTCAC CTTGAGGTCC 2280
 CCTCGCCCCG TCACACCGTT ATCGATTACT CTGTGTCTAC TATTATGTGT GCATAATTTA 2340
 TACCGTAAAT GTTTACTCTT TAAATAAAAA AAAAAAAAAA 2380

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Gly	Leu	Gly	Arg	Val	Leu	Leu	Phe	Leu	Ala	Val	Ala	Phe	Pro	Phe
1				5				10					15		
Ala	Pro	Pro	Ala	Ala	Ala	Ala	Glu	Pro	His	Ser	Leu	Arg	Tyr	Asn	Leu
			20				25						30		

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Met Val Leu Ser Gln Asp Glu Ser Val Gln Ser Gly Phe Leu Ala Glu
35 40 45

Gly His Leu Asp Gly Gln Pro Phe Leu Arg Tyr Asp Arg Gln Lys Arg
50 55 60

Arg Ala Lys Pro Gln Gly Gln Trp Ala Glu Asp Val Leu Gly Ala Lys
65 70 75 80

Thr Trp Asp Thr Glu Thr Glu Asp Leu Thr Glu Asn Gly Gln Asp Leu
85 90 95

Arg Arg Thr Leu Thr His Ile Lys Asp Gln Lys Gly Gly Leu His Ser
100 105 110

Leu Gln Glu Ile Arg Val Cys Glu Ile His Glu Asp Ser Ser Thr Arg
115 120 125

Gly Ser Arg His Phe Tyr Tyr Asp Gly Glu Leu Phe Leu Ser Gln Asn
130 135 140

Leu Glu Thr Gln Glu Ser Thr Val Pro Gln Ser Ser Arg Ala Gln Thr
145 150 155 160

Leu Ala Met Asn Val Thr Asn Phe Trp Lys Glu Asp Ala Met Lys Thr
165 170 175

Lys Thr His Tyr Arg Ala Met Gln Ala Asp Cys Leu Gln Lys Leu Gln
180 185 190

Arg Tyr Leu Lys Ser Gly Val Ala Ile Arg Arg Thr Val Pro Pro Met
195 200 205

Val Asn Val Thr Cys Ser Glu Val Ser Glu Gly Asn Ile Thr Val Thr
210 215 220

Cys Arg Ala Ser Ser Phe Tyr Pro Arg Asn Ile Thr Leu Thr Trp Arg
225 230 235 240

Gln Asp Gly Val Ser Leu Ser His Asn Thr Gln Gln Trp Gly Asp Val
245 250 255

Leu Pro Asp Gly Asn Gly Thr Tyr Gln Thr Trp Val Ala Thr Arg Ile
260 265 270

Arg Gln Gly Glu Glu Gln Arg Phe Thr Cys Tyr Met Glu His Ser Gly
275 280 285

Asn His Gly Thr His Pro Val Pro Ser Gly Lys Val Leu Val Leu Gln
290 295 300

Ser Gln Arg Thr Asp Phe Pro Tyr Val Ser Ala Ala Met Pro Cys Phe
305 310 315 320

Val Ile Ile Ile Ile Leu Cys Val Pro Cys Cys Lys Lys Lys Thr Ser
325 330 335

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Ala Ala Glu Gly Pro Glu Leu Val Ser Leu Gln Val Leu Asp Gln His
 340 345 350

Pro Val Gly Thr Gly Asp His Arg Asp Ala Ala Gln Leu Gly Phe Gln
 355 360 365

Pro Leu Met Ser Ala Thr Gly Ser Thr Gly Ser Thr Glu Gly Ala
 370 375 380

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ACTGGGGAAC AAGGTTTATA TGAGA

25

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TGTCACCCGT CTTCTACAGG ACCC

24

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGGGCCATGG GGCTGGG

17

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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ATCTGAGATG TCGGTCC

17

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CGTTCTTGTC CCTTTGCCCCG TGTGC

25

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AACCCTTCCC TTACCCCCGT CGTAG

25

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TATGTAAAAC GACGGCCAGT TTCACCTGTG ATTCCTCTT CCCCA

45

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGTCTTTTCA ATCCCCGTCT CTCGTCCAGT ATCGACAAAG GACAT

45

(2) INFORMATION FOR SEQ ID NO: 13:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TATGTAAAAC GACGGCCAGT TTCGGAATG GAGAAATCAC

40

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CGAGAGGAGA GGGAGGTAA CCAGTATCGA CAAAGGACAT

40

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TATGTAAAAC GACGGCCAGT GTTCCTCTCC CCTCCTTAGA

40

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

AAAAAGTCCC TTTCACGACC ACCAGTATCG ACAAAGGACA T

41

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